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## ARTICLE

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### Large scale cDNA sequencing for analysis of quantitative and qualitative aspects of gene expression

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**Large scale sequencing of cDNAs provides a complementary approach to structural analysis of the human genome by generating expressed sequence tags (ESTs). We have initiated the large-scale sequencing of a 3'-directed cDNA library from the human liver cell line HepG2, that is a non-biased representation of the mRNA population. 982 random cDNA clones were sequenced yielding more than 270 kilobases. A significant portion of the identified genes encoded secreted proteins and components for protein-synthesis. The abundance of cDNA species varied from 2.2% to less than 0.004%. Fifty two percent of the mRNA were abundant species consisting of 173 genes and the rest were non-abundant, consisting of about 6,600 genes.**

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## ABSTRACT

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